

Application No. 09/808,225
Filed: March 14, 2001
TC Art Unit: 1645
Confirmation No.: 2805

AMENDMENT TO THE CLAIMS

1. (Previously Presented) A process for identifying and enriching cell-specific target structures, in particular for the identification of cell-specific protein combination patterns on a surface of cells and for enriching such cells, wherein said process comprises the following steps:

(a) depositing a heterogeneous cell mixture on one or plural surfaces with predefined structures, causing cells with corresponding target structures to become bound to such surface(s);

(b) removing any non-binding cells of said cell mixture from said surface(s);

(c) identifying the cell-specific target structures responsible for the binding of the cells to said surface(s);

(d) selecting and enriching cells with identical cell-specific target structures on said surface(s); and

(e) biochemically characterizing the target structures selected in procedural step (d).

2. (Original) The process as claimed in claim 1 wherein said heterogeneous cell mixture has been isolated from human or animal tissue or human or animal body fluids, or it consists of cultivated cells.

3. (Previously Presented) The process as claimed in claim 1 wherein said surface is a human or animal tissue section and/or endothelioid cells and/or protein chips and/or a cultivated piece of human or animal tissue.

PROCESS FOR IDENTIFYING AND ENRICHING
CELL-SPECIFIC TARGET STRUCTURES

5 DESCRIPTION:

 The present invention relates to a process for
identifying and enriching cell-specific target
structures, in particular for the identification of
10 cell-specific protein combination patterns on cell
surfaces and for enriching such cells.

 Identifying cell-specific target structures is
crucial for elucidating cell-to-cell interactions which
may cause countless effects within an organism.
15 Especially, knowing disease-specific target structures
is a decisive prerequisite for developing effective
drugs which at the same time only have few side effects.

 It is known from the prior art that immune cells
(lymphocytes) will express specific combinations of
20 proteins, also referred to as protein combination
patterns or, in short, PCP, which are responsible for
binding to endothelioid cells of the blood vessels in
the brain and in muscle tissue. Other protein
combinations, however, will not result in any binding to
25 such endothelioid cells. Surprisingly, these specific
combinations are inter-individually consistent, always
exhibiting the same binding functions. Consequently,
the specific protein combination patterns seem to be an
inter-individually consistent lymphocyte binding code of
30 the cell surface for organ-specific endothelioid cell
surfaces which represents a cell-specific target
structure. Cell-specific target structures may thus
exhibit quite specific protein combination patterns.

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4. (Previously Presented) The process as claimed in claim 1 wherein the cell-specific target structures are identified in a process comprising the following steps:

(I) automatically depositing a reagent solution Y1 that includes at least one marker molecule on said cell-specific target structure;

(II) allowing the reagent solution Y1 to react, and automatically detecting at least one marker pattern of the target structure labeled with the reagent solution Y1;

(III) removing said reagent solution Y1 before or after detecting the marker pattern, and repeating steps (I) and (II) with further reagent solutions Yn (n = 2, 3, ..., N) each containing said at least one marker molecule and/or at least another marker molecule; and

(IV) combining the marker patterns detected in step (II) to give a complex molecular combination pattern of the cell-specific target structure.

5. (Currently Amended) The process as claimed in claim 1 wherein the selected target structures are biochemically characterized in procedural step (e) by means of a molecule or a molecular complex separation process.

6. (Previously Presented) The process as claimed in claim 13 wherein said protein separation process is 2D gel electrophoresis.

7. (Currently Amended) The process as claimed in claim 1 wherein the following procedural step is performed after procedural step (d):

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(d1) conducting inhibition experiments regarding one or plural ingredients of the cell-specific target structures selected in procedural step (d) for detecting a binding hierarchy of the ingredients.

8. (Original) The process as claimed in claim 7 wherein said ingredients are single or plural proteins of a cell-specific protein combination pattern.

9. (Currently Amended) The process as claimed in claim 1 wherein procedural step (e) comprises the steps of:

automatically depositing a reagent solution Y1 that includes at least one marker molecule on said selected and enriched cell-specific target structure;

allowing the reagent solution Y1 to react, and automatically detecting at least one marker pattern of the target structure labeled with the reagent solution Y1;

removing said reagent solution Y1 before or after detecting the marker pattern, and repeating steps (f) and (g) with further reagent solutions Yn (n = 2, 3, ..., N) each containing said at least one marker molecule and/or at least another marker molecule; and

combining the marker patterns detected in step (g) to give a complex molecular combination pattern of the selected and enriched cell-specific target structure.

10. (Previously Presented) The process as claimed in claim 2 wherein said surface is a human or animal tissue section and/or endothelioid cells and/or protein chips and/or a cultivated piece

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of human or animal tissue, and the cell-specific target structures are identified in a process comprising the following steps:

(I) automatically depositing a reagent solution Y1 that includes at least one marker molecule on said cell-specific target structure;

(II) allowing the reagent solution Y1 to react, and automatically detecting at least one marker pattern of the target structure labeled with the reagent solution Y1;

(III) removing said reagent solution Y1 before or after detecting the marker pattern, and repeating steps (I) and (II) with further reagent solutions Yn ($n = 2, 3, \dots, N$) each containing said at least one marker molecule and/or at least another marker molecule;

(IV) combining the marker patterns detected in step (II) to give a complex molecular combination pattern of the cell-specific target structure;

(V) biochemically characterizing the selected target structures by means of 2D gel electrophoresis; and

(VI) conducting inhibition experiments regarding one or plural ingredients of the cell-specific target structures selected in procedural step (d) for detecting a binding hierarchy of the ingredients.

11. (Previously Presented) The process as claimed in claim 10 wherein said ingredients are single or plural proteins of a cell-specific protein combination pattern.

12. (Previously Presented) A process for identifying and enriching cell-specific target structures, in particular for the

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identification of cell-specific protein combination patterns on the surface of cells and for enriching such cells, wherein said process comprises the following steps:

(a) depositing a heterogeneous cell mixture on one or plural surfaces with predefined structures, causing cells with corresponding target structures to become bound to such surface(s);

(b) removing any non-binding cells of said cell mixture from said surface(s);

(c) identifying the cell-specific target structures responsible for the binding of the cells to said surface(s);

(d) selecting and enriching cells with identical cell-specific target structures on said surface(s);

(e) automatically depositing a reagent solution Y1 that includes at least one marker molecule on said selected and enriched cell-specific target structure;

(f) allowing the reagent solution Y1 to react, and automatically detecting at least one marker pattern of the target structure labeled with the reagent solution Y1;

(g) removing said reagent solution Y1 before or after detecting the marker pattern, and repeating steps (a) and (b) with further reagent solutions Yn (n = 2, 3, ..., N) each containing said at least one marker molecule and/or at least another marker molecule; and

(h) combining the marker patterns detected in step (b) to give a complex molecular combination pattern of the selected and enriched cell-specific target structure.

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13. (Previously Presented) The process as claimed in claim 5 wherein the molecule or molecular complex separation process is a protein separation process.

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